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<i>2/52</i>  <i>Fig.1(i)</i>	<i>3/52</i>  <i>Fig.1(ii)</i>
<i>4/52</i>  <i>Fig.1(iii)</i>	<i>5/52</i>  <i>Fig.1(iv)</i>

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1	TCGGCCTCC GAAACC ATG AAC TTT CTG	
	Met Asn Phe Leu	1
50	CTT GCC TTG CTG CTC TAC CTC CAC	
	Leu Ala Leu Leu Leu Tyr Leu His	15
98	CCC ATG GCA GAA GGA GGA GGG CAG	
	Pro Met Ala Glu Gly Gly Gly Gln	30 35
146	ATG GAT GTC TAT CAG CGC AGC TAC	
	Met Asp Val Tyr Gln Arg Ser Tyr	45 50
194	GAC ATC TTC CAG GAG TAC CCT GAT	
	Asp Ile Phe Gln Glu Tyr Pro Asp	60 65
242	TCC TGT GTG CCC CTG ATG CGA TGC	
	Ser Cys Val Pro Leu Met Arg Cys	80
290	CTC GAG TGT GTG CCC ACT GAG GAG	
	Leu Glu Cys Val Pro Thr Glu Glu	95
338	CGG ATC AAA CCT CAC CAA GGC CAG	
	Arg Ily Lys Pro His Gln Gly Gln	110 115

Fig.1(i)

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CTG	TCT	TGG	GTG	CAT	TGG	AGC		49
Leu	Ser	Trp	Val	His	Trp	Ser		
5					10			
CAT	GCC	AAG	TGG	TCC	CAG	GCT	GCA	97
His	Ala	Lys	Trp	Ser	Gln	Ala	Ala	
20					25			
AAT	CAT	CAC	GAA	GTG	GTG	AAG	TTC	145
Asn	His	His	Glu	Val	Val	Lys	Phe	
			40					
TGC	CAT	CCA	ATC	GAG	ACC	CTG	GTG	193
Cys	His	Pro	Ile	Glu	Thr	Leu	Val	
			55					
GAG	ATC	GAG	TAC	ATC	TTC	AAG	CCA	241
Glu	Ile	Glu	Tyr	Ile	Phe	Lys	Pro	
		70					75	
GGG	GGC	TGC	TGC	AAT	GAC	GAG	GGC	289
Gly	Gly	Cys	Cys	Asn	Asp	Glu	Gly	
	85					90		
TCC	AAC	ATC	ACC	ATG	CAG	ATT	ATG	337
Ser	Asn	Ile	Thr	Met	Gln	Ile	Met	
100					105			
CAC	ATA	GGA	GAG	ATG	AGC	TTC	CTA	385
His	Ile	Gly	Glu	Met	Ser	Phe	Leu	
			120					

Fig.1(ii)

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386	CAG CAC AAC AAA TGT GAA TGC AGA	
	Gln His Asn Lys Cys Glu Cys Arg	
	125	130
434	GAA AAT CCC TGT GGG CCT TGC TCA	
	Glu Asn Pro Cys Gly Pro Cys Ser	
	140	145
482	CAA GAT CCG CAG ACG TGT AAA TGT	
	Gln Asp Pro Gln Thr Cys Lys Cys	
		160
530	TGC AAG GCG AGG CAG CTT GAG TTA	
	Cys Lys Ala Arg Gln Leu Glu Leu	
		175
578	AAG CCG AGG CGG TGAGCCGGGC AGGAG	
	Lys Pro Arg Arg	
		190
630	GAACCAGATC TCTCACCAGG	

*Fig.1(iii)*

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CCA AAG AAA GAT AGA GCA AGA CAA	433
Pro Lys Lys Asp Arg Ala Arg Gln	
135	
GAG CGG AGA AAG CAT TTG TTT GTA	481
Glu Arg Arg Lys His Leu Phe Val	
150 155	
TCC TGC AAA AAC ACA GAC TCG CGT	529
Ser Cys Lys Asn Thr Asp Ser Arg	
165 170	
AAC GAA CGT ACT TGC AGA TGT GAC	577
Asn Glu Arg Thr Cys Arg Cys Asp	
180 185	
GAAGG AGCCTCCCTC AGCGTTTCGG	629

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Fig.1(iv)

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7/52  Fig. 2(i)	8/52  Fig. 2(ii)
9/52  Fig 2(iii)	10/52  Fig 2(iv)
11/52  Fig 2(v)	12/52  Fig 2(vi)

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1	CC ATG AGC CCT CTG CTC CGC CGC
	Met Ser Pro Leu Leu Arg Arg
	1 5
48	CTG GCC CCC GCC CAG GCC CCT GTC
	Leu Ala Pro Ala Gln Ala Pro Val
	20
96	CAG AGG AAA GTG GTG TCA TGG ATA
	Gln Arg Lys Val Val Ser Trp Ile
	35
144	CAG CCC CGG GAG GTG GTG GTG CCC
	Gln Pro Arg Glu Val Val Val Pro
	50 55
192	GTG GCC AAA CAG CTG GTG CCC AGC
	Val Ala Lys Gln Leu Val Pro Ser
	65 70
240	GGC TGC TGC CCT GAC GAT GGC CTG
	Gly Cys Cys Pro Asp Asp Gly Leu
	80 85
288	CAA GTC CGG ATG CAG ATC CTC ATG
	Gln Val Arg Met Gln Ile Leu Met
	100
336	GGG GAG ATG TCC CTG GAA GAA CAC
	Gly Glu Met Ser Leu Glu Glu His
	115

Fig.2(i)

[illegible]

*Fig. 2(ii)*



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384	AAA	AAG	GAC	AGT	GCT	GTG	AAG	CCA
	Lys	Lys	Asp	Ser	Ala	Val	Lys	Pro
			130					135
432	CGT	CCC	CAG	CCC	CGT	TCT	GTT	CCG
	Arg	Pro	Gln	Pro	Arg	Ser	Val	Pro
		145					150	
480	CCC	TCC	CCA	GCT	GAC	ATC	ACC	CAT
	Pro	Ser	Pro	Ala	Asp	Ile	Thr	His
	160					165		
528	GCC	CAC	GCT	GCA	CCC	AGC	ACC	ACC
	Ala	His	Ala	Ala	Pro	Ser	Thr	Thr
					180			
576	GCT	GCC	GCT	GCC	GAC	GCC	GCA	GCT
	Ala	Ala	Ala	Ala	Asp	Ala	Ala	Ala
				195				

Fig. 2(iii)

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GAC	AGG	GCT	GCC	ACT	CCC	CAC	CAC	431
Asp	Arg	Ala	Ala	Thr	Pro	His	His	
				140				
GGC	TGG	GAC	TCT	GCC	CCC	GGA	GCA	479
Gly	Trp	Asp	Ser	Ala	Pro	Gly	Ala	
				155				
CCC	ACT	CCA	GCC	CCA	GGC	CCC	TCT	527
Pro	Thr	Pro	Ala	Pro	Gly	Pro	Ser	
			170				175	
AGC	GCC	CTG	ACC	CCC	GGA	CCT	GCC	575
Ser	Ala	Leu	Thr	Pro	Gly	Pro	Ala	
			185				190	
TCC	TCC	GTT	GCC	AAG	GGC	GGG	GCT	T 624
Ser	Ser	Val	Ala	Lys	Gly	Gly	Ala	
200					205			

Fig.2(iv)

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625 AGAGCTCAAC CCAGACACCT GCAGGTGCCG  
685 GACTCAGCAG GGTGACTTGC CTCAGAGGCT  
745 GGTA AAAAAC AGCCAAGCCC CCAAGACCTC  
805 GCCTCTCAGA GGGCTCTTCT GCCATCCCTT  
865 GAGTTGGAAG AGGAGACTGG GAGGCAGCAA  
825 GGAGTACTGT CTCAGTTTCT AACCACTCTG  
985 CTCCCCTCAC TAAGAAGACC CAAACCTCTG  
1045 CTGTGACCCC CAACCCTGAT AAAAGAGATG

*Fig.2(v)*

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GAAGCTGCGA AGGTGACACA TGGCTTTTCA	684
ATATCCCAGT GGGGGAACAA AGGGGAGCCT	744
AGCCCAGGCA GAAGCTGCTC TAGGACCTGG	804
GTCTCCCTGA GGCCATCATC AAACAGGACA	864
GAGGGGTCAC ATACCAGCTC AGGGGAGAAT	924
TGCAAGTAAG CATCTTACAA CTGGCTCTTC	984
CATAATGGGA TTTGGGCTTT GGTACAAGAA	1044
GAAGGAAAAA AAAAAAAAAA	1094

*Fig.2(vi)*

[illegible]

Fig.3(ii)

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>VEGF\_HUMAN VEGF\_HUMAN VASCULAR ENDOTHELIAL  
(VASCULAR 215 AA.  
LENGTH = 215

SCORE = 181 (92.4 BITS), EXPECT =  $6.4e-20$ ,  
IDENTITIES = 33/75 (44%), POSITIVES = 48/75

QUERY: 31 HQRKVVSVIDVYTRATCQPREVVVPLTVEL  
+++ VV +DVY R+ C+P E +V + E  
SBJCT: 36 NHHEVVKFMDVYQRSYCHPIETLVDIFQEY

QUERY: 91 PTGQHQVRMQILMIR 105  
PT + + MQI+ I+  
SBJCT: 96 PTEESNITMQIMRIK 110

SCORE = 76 (38.8 BITS), EXPECT = 0.0011,  
IDENTITIES = 12/19 (63%), POSITIVES = 16/19

QUERY: 110 QLGEMSLEEHSQCECRPKK 128  
++GEMS +H+ CECRPKK  
SBJCT: 116 HIGEMSFLQHNKCECRPKK 134

SCORE = 72 (36.8 BITS), EXPECT = 0.0046,  
IDENTITIES = 14/21 (66%), POSITIVES = 15/21

QUERY: 202 RCQGRGLELNPDTCTCRCLRR 222  
RC +R LELN TCRC K RR  
SBJCT: 195 RCKARQLELNERTCRCDKPRR 215

SCORE = 46 (23.5 BITS), EXPECT = 47.,  
IDENTITIES = 6/10 (60%), POSITIVES = 9/10

QUERY: 187 DPRTCTCRCCR 196  
DP+TC+C C+  
SBJCT: 181 DPQTCKCSCK 190

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Fig.3(i)

Fig.3(i) 20040000

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GROWTH FACTOR PRECURSOR (VEGF)

 $P = 6.4e-20$   
(64%) $MGTVAKQLVPSCVTVQRCGGCCPDDGLECV$  90  
+  $PSCV + RCGGCC D+GLECV$   
 $PDEIEYIFKPSCVPLMRCGGCCNDEGLECV$  95POISSON  $P(2) = 9.1e-12$   
(84%)POISSON  $P(3) = 3.6e-18$   
(71%)POISSON  $P(4) = 7.3e-10$   
(90%)*Fig. 3(i)*

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17/52  <i>Fig. 4(i)</i>	18/52  <i>Fig. 4(ii)</i>
19/52  <i>Fig. 4(iii)</i>	20/52  <i>Fig. 4(iv)</i>



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TGCTCGCCGCACT.....CC	67
...TGGGTGCATTGGAGCCTTGCCT	56
TGTCTCCCAGCCTGATGCCCTGGC	117
GTGGTCCCAGGCTGCA.CCCATGGC	105
.AAGTGGTG....TCATGGATAGAT	147
GAAGTGGTGAAGTTCATG....GAT	151
CCCCGGGAG...GTGGTGGTGCCCT	193
CCAATCGAGACCCTGGTGGACATCT	200
GGGCACCGTGGCCAAACAGCTGGTG	234
GTACATCTT...CAA.....G	238
GTGGTGGCTGCTGCCCTGACGATGG	284
GCGGGGGGCTGCTGCAATGACGAGGG	288
CACCAAGTCCGGATGCAGAT.....	329
TCCAACATCACCATGCAGATTATGC	338

Fig. 4(ii)  
SUBSTITUTE SHEET (RULE 26)

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Gap Weight:3.00      Average Match:1.000  
 Length Weight:0.100      Average Mismatch:-0.900  
 Quality:100.9      Length:739  
 Ratio:0.175      Gaps:30  
 Percent      Percent  
 Similarity:69.703      Identity:69.703

```

28   ATGAGCCCTCTGCTCCGCCGCCTGC
      |||| | ||||| | ||
17   ATGAACTTTCTGCT.....GTCT..

68   TGCAGCTGGCCCCCGCCCAGGCCCC
      ||| ||| || | ||| |||
57   TGCTGCTCTACCTCCACCATGCCAA

118  CACCAGAGGA.....
      |||||
106  AGAAGGAGGAGGGCAGAATCATCAC

140  GTGTATACTCGC.GCTACCTGCCAG
      || ||| ||| |||| |||||
152  GTCTATCAGCGCAGCTA.CTGCCAT

194  T....GA.....CTGTGGAGCTCAT
      | || ||| ||| ||
201  TCCAGGAGTACCCTGATGAGATCGA

235  CCCAGCTGCGTGACTGTGCAGCGCT
      || ||| ||| | || ||| |
239  CCATCCTGTGTGCCCCTGATGCGAT

285  CCTGGAGTGTGTGCCCCACTGGGCAG
      ||||| ||||| ||||| ||| ||
289  CCTGGAGTGTGTGCCCCACTGAGGAG
  
```

Fig.4(i)

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19/52

330 .....CCTCATGATCCGGTACC  
                   |||||  
 339 GGATCAAACCTCA.....C  
  
 369 GTCCCTGGAAGAACACAGCCAGTGT  
      |  |  |  |  |  |  |  |  |  |  
 376 GAGCTTCCTACAGCACAAATGT  
  
 419 GTGCTGTGAAGCCAGACAGGGCTGC  
      |          |||  |||||  |  
 423 G.....AGCAAGACAAG.....  
  
 469 CGTTCTGTTCCGGGCTGGGACTCTG  
      |  |  |  |  |  |  |  |  
 443 ...TGTGGGCCTTGCTCAGA.....  
  
 519 CATCACCCATCCCACTCCAGCCCCA  
  
 468 .....  
  
 569 GC.....ACCACCAGCGCCC  
      ||          |||  
 469 GCATTTGTTTGTACAA.....  
  
 609 TGCCGACGCCGCAGCTTCCTCCGTT  
      ||  |  |  |  |  |  |  |  |  
 509 TG.CAAAAACACAGACTC..GCGTT  
  
 657 AACCCAGACACCTGCAGGTGCCGGA  
      |||  |  
 554 AACGAACGTACTTGCAGATGTGACA

Fig.4(iii)

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CGAGCAGTCAGC...TGGGGGAGAT	368
CAAG...GCCAGCACATAGGAGAGAT	375
GAATGCAGACCTAAAAAAAGGACA	418
GAATGCAGACC...AAAGAAAGATA	422
CACTCCCCACCACCGTCCCCAGCCC	468
.....AAAATCCC.....	442
CCCCCGGAGCACCTCCCCAGCTGA	518
...GCGGAGAA.....	467
GGCCCCTCTGCCCACGCTGCACCCA	568
.....A	468
TGACCCCCGGACCTGCCGCTGCCGC	608
.GATCCGCAGACGTGTAAATGTTCC	508
GCCAAGGGCGGGGC..TTAGAGCTC	656
GC..AAGGCGAGGCAGCTTGAGTTA	553
AGCTGCGAAGGTGA	695
AGCCGAGGCGGTGA	592

Fig.4(iv)

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22/52 <sup>*</sup>  <i>Fig. 5(i)</i>	23/52  <i>Fig. 5(ii)</i>	24/52  <i>Fig. 5(iii)</i>
25/52  <i>Fig. 5(iv)</i>	26/52  <i>Fig. 5(v)</i>	27/52  <i>Fig. 5(vi)</i>

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165SOMSQ.MSF.msf MSF:687

Type: D Tuesday, June 20, 1995

Check:3140

	1
VEGF165	ATGAACTTTCTGCTGTCTTGGGTG
SOM175	ATGAGCCCTCTGCTCCGCCGCCTG
SOM175-e6	ATGAGCCCTCTGCTCCGCCGCCTG
SOM175-e6&7	ATGAGCCCTCTGCTCCGCCGCCTG
SOM175-e4	ATGAGCCCTCTGCTCCGCCGCCTG
	81
VEGF165	CACCCATGGCAGAAGGAGGAGGGC
SOM175	TGCCCCTGGCCACCAGAGGAAAGT
SOM175-e6	TGCCCCTGGCCACCAGAGGAAAGT
SOM175-e6&7	TGCCCCTGGCCACCAGAGGAAAGT
SOM175-e4	TGCCCCTGGCCACCAGAGGAAAGT
	161
VEGF165	CCAATCGAGACCCTGGTGGACATC
SOM175	GTGGTGGTGCCCTTGACTG.TGGA
SOM175-e6	GTGGTGGTGCCCTTGACTG.TGGA
SOM175-e6&7	GTGGTGGTGCCCTTGACTG.TGGA
SOM175-e4	GTGGTGGTGCCCTTGACTG.TGGA
	241
VEGF165	GATGCGATGCGGGGGCTGCTGCAA
SOM175	GCAGCGCTGTGGTGGCTGCTGCCC
SOM175-e6	GCAGCGCTGTGGTGGCTGCTGCCC
SOM175-e6&7	GCAGCGCTGTGGTGGCTGCTGCCC
SOM175-e4	GCAGCGCTGTGGTGGCTGCTGCCC

Fig.5(i)

SUBSTITUTE SHEET (RULE 26)

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CATTGGAGCCTTGCCTTGCTGCTCTACC  
CTGCTCGCCGCACTCCTGCAGCTGGCCC  
CTGCTCGCCGCACTCCTGCAGCTGGCCC  
CTGCTCGCCGCACTCCTGCAGCTGGCCC  
CTGCTCGCCGCACTCCTGCAGCTGGCCC

AGAATCATCACGAAGTGGTGAAGTTCAT  
GGTGTTCATGGATAGATGTGTATACTCGC  
GGTGTTCATGGATAGATGTGTATACTCGC  
GGTGTTCATGGATAGATGTGTATACTCGC  
GGTGTTCATGGATAGATGTGTATACTCGC

TTCCAGGAGTACCCTGATGAGATCGAGT  
GCTCATGGGCACCGTGGCCAAAC..AGC  
GCTCATGGGCACCGTGGCCAAAC..AGC  
GCTCATGGGCACCGTGGCCAAAC..AGC  
GCTCATGGGCACCGTGGCCAAAC..AGC

TGACGAGGGCCTGGAGTGTGTGCCCCACT  
TGACGATGGCCTGGAGTGTGTGCCCCACT  
TGACGATGGCCTGGAGTGTGTGCCCCACT  
TGACGATGGCCTGGAGTGTGTGCCCCACT  
TGACGATGGCCTGGAGTGTGTGCCCCACT

*Fig.5(ii)*

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80

TCCACCATGCCAAGTGGTCCCAGGCTG.  
CCGCCCAGGCCCTGTCTCCCAGCCTGA  
CCGCCCAGGCCCTGTCTCCCAGCCTGA  
CCGCCCAGGCCCTGTCTCCCAGCCTGA  
CCGCCCAGGCCCTGTCTCCCAGCCTGA

160

GGATGTCTATCAGCGCAGCTACTGCCAT  
G.....CTACCTGC.CAGCC.CCGGGAG  
G.....CTACCTGC.CAGCC.CCGGGAG  
G.....CTACCTGC.CAGCC.CCGGGAG  
G.....CTACCTGC.CAGCC.CCGGGAG

240

ACATCTTCAAGCCATCCTGTGTGCCCCCT  
TGGTGCCCAG.....CTGCGTGACTGT  
TGGTGCCCAG.....CTGCGTGACTGT  
TGGTGCCCAG.....CTGCGTGACTGT  
TGGTGCCCAG.....CTGCGTGACTGT

320

GAGGAGTCCAACATCACCATGCAGATTA  
GGGCAGCACCAAGTCCGGATGCAGATCC  
GGGCAGCACCAAGTCCGGATGCAGATCC  
GGGCAGCACCAAGTCCGGATGCAGATCC  
GGGCAGCACCAAGTCCGGATGCAGA...

*Fig.5(iii)*



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321  
VEGF165 TGCGGATCAAACCTCACCAAGGCC  
SOM175 TCATGATCCGG...TACCCGAGCA  
SOM175-e6 TCATGATCCGG...TACCCGAGCA  
SOM175-e6&7 TCATGATCCGG...TACCCGAGCA  
SOM175-e4 .....

401  
VEGF165 AAGAAAGATAG.....AGCAA  
SOM175 AAAAAGGACAGTGCTGTGAAGCCA  
SOM175-e6 AAAAAGGACAGTGCTGTGAAGCCA  
SOM175-e6&7 AAAAAGGACAGTGCTGTGAAGCCA  
SOM175-e4 AAAAAGGACAGTGCTGTGAAGCCA

481  
VEGF165 .....AAGCA.....  
SOM175 CTCTGCCCCCGGAGCACCCCTCCCC  
SOM175-e6 .....  
SOM175-e6&7 .....  
SOM175-e4 CTCTGCCCCCGGAGCACCCCTCCCC

561  
VEGF165 A.....GATCCGCA  
SOM175 GCACCACCAGCGCCCTGACCCCCG  
SOM175-E6 GCACCACCAGCGCCCTGACCCCCG  
SOM175-e6&7 .....  
SOM175-e4 GCACCACCAGCGCCCTGACCCCCG

641  
VEGF165 TTGAGTTAAACGAACGTACTTGCA  
SOM175 TAGAGCTCAACCCAGACACCTGCA  
SOM175-e6 TAGAGCTCAACCCAGACACCTGCA  
SOM175-e6&7 .....  
SOM175-e4 TAGAGCTCAACCCAGACACCTGCA

*Fig.5(iv)*

T E G A C C C G G A G C A C C C T C C C C

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AGCACATAGGAGAGATGAGCTTCCTACA  
GTCAGCTGGGGGAGATGTCCCTGGAAGA  
GTCAGCTGGGGGAGATGTCCCTGGAAGA  
GTCAGCTGGGGGAGATGTCCCTGGAAGA  
.....

GACAAGAA....AATCCCTGTGG.....  
GACAGGGCTGCCACTCCCCACCACCGTC  
GATAG.....  
GATAG.....  
GACAGGGCTGCCACTCCCCACCACCGTC

.....  
AGCTGACATCACCCATCCCACTCCAGCC  
.....CC  
.....  
AGCTGACATCACCCATCCCACTCCAGCC

GACGTGTAAATGTTCTGCAAAAAC.AC  
GACCTGCCGCTGCCGCTGCCGACGCCGC  
GACCTGCCGCTGCCGCTGCCGACGCCGC  
.....  
GACCTGCCGCTGCCGCTGCCGACGCCGC

687

GATGTGACAAGCCGAGGCGGTGA  
GGTGCCGGAAGCTGCGAAGGTGA  
GGTGCCGGAAGCTGCGAAGGTGA  
.GTGCCGGAAGCTGCGAAGGTGA  
GGTGCCGGAAGCTGCGAAGGTGA

*Fig.5(v)*

T02F02020600

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400

GCACAACAAATGTGAATGCAGACC...A  
ACACAGCCAGTGTGAATGCAGACCTAAA  
ACACAGCCAGTGTGAATGCAGACCTAAA  
ACACAGCCAGTGTGAATGCAGACCTAAA  
.....CCTAAA

480

.....GCCTTGCTCAGAGCGGAGA  
CCCAGCCCCGTTCTGTTCCGGGCTGGGA  
.....  
.....  
CCCAGCCCCGTTCTGTTCCGGGCTGGGA

560

.....TTTGTT.....TGTAC..A  
CCAGGCCCCCTCTGCCCACGCTGCACCCA  
CCAGGCCCCCTCTGCCCACGCTGCACCCA  
.....  
CCAGGCCCCCTCTGCCCACGCTGCACCCA

640

AGACTCG..CGTTGCAAGGCGAGGCAGC  
AGCTTCCTCCGTTGCCAAGGGCGGGGCT  
AGCTTCCTCCGTTGCCAAGGGCGGGGCT  
.....  
AGCTTCCTCCGTTGCCAAGGGCGGGGCT

Fig.5(vi)

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<i>Fig 6(i)</i>	29/52	<i>Fig 6(ii)</i>	30/52
<i>Fig 6(iii)</i>	31/52		

09607007 024204

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PCT/AU96/00094

VEGF <sub>165</sub>	M	N	F	L	L	S	W	V	H	W	S	L	A	L	A	L	L	Y	L	H	H	A	K	W	S	Q	A	A	P
SOM175 <sub>Short</sub>	M	S	P	L	L	R	R	L	L	.	.	L	A	A	L	L	L	Q	L	A	P	A	Q	.	.	.	.	A	P
VEGF <sub>165</sub>	I	F	Q	E	Y	P	D	E	I	E	Y	I	F	K	P	S	C	V	P	L	M	R	C	G	G	C	C	N	
SOM175 <sub>Short</sub>	L	T	V	E	L	M	G	T	V	A	K	Q	L	V	P	S	C	V	T	V	Q	R	C	G	3	C	C	P	
VEGF <sub>165</sub>	F	L	Q	H	N	K	C	E	C	R	P	K	K	.	.	.	.	.	.	.	D	R	A	.	.	.	.	.	
SOM175 <sub>Short</sub>	L	E	E	H	S	Q	C	E	C	R	P	K	K	K	D	S	A	V	K	P	D	R	A	A	T	P	H		
VEGF <sub>165</sub>	C	K	C	S	C	K	N	T	D	S	R	C	K	A	R	Q	L	E	L	N	E	R	T	C	R	C	D	K	
SOM175 <sub>Short</sub>	H	A	A	P	S	T	S	A	L	T	P	G	P	A	A	A	A	A	A	D	A	A	S	S	V	A	K		
OR...																													
VEGF <sub>165</sub>	M	N	F	L	L	S	W	V	H	W	S	L	A	L	A	L	L	Y	L	H	H	A	K	W	S	Q	A	A	P
SOM175 <sub>Long</sub>	M	S	P	L	L	R	R	L	L	.	.	L	A	A	L	L	L	Q	L	A	P	A	Q	.	.	.	.	A	P
VEGF <sub>165</sub>	I	F	Q	E	Y	P	D	E	I	E	Y	I	F	K	P	S	C	V	P	L	M	R	C	G	G	C	C	N	
SOM175 <sub>Long</sub>	L	T	V	E	L	M	G	T	V	A	K	Q	L	V	P	S	C	V	T	V	Q	R	C	G	G	C	C	P	
VEGF <sub>165</sub>	F	L	Q	H	N	K	C	E	C	R	P	K	K	.	.	.	.	.	.	.	D	R	A	.	.	.	.	.	
SOM175 <sub>Long</sub>	L	E	E	H	S	Q	C	E	C	R	P	K	K	K	D	S	A	V	K	P	D	R	A	A	T	P	H		
VEGF <sub>165</sub>	G	P	C	S	E	R	R	K	H	L	F	V	Q	D	P	Q	T	C	K	C	S	C	K	N	T	D	S	.	
SOM175 <sub>Long</sub>	P	R	C	T	Q	H	H	Q	R	.	.	P	D	P	D	P	R	T	C	R	C	R	C	R	R	R	S	F	L

Fig.6(i)

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M A E G G G Q N	H H E .	V V K F M	D V Y Q R S Y	C H P I E T L	V D	60
V S Q P D A P G	H Q R K	V V S W I	D V Y T R A T C C P R E	V V V	P	55
D E G L E C V P T	E E S N I	T M Q I M R I	K P H Q G Q H I	G E M S	121	
D D G L E C V P T	G Q H Q V	R M Q I L M I	Y P S S Q L	G E M S	115	
. . . . .	R Q E N	P C G P C S E R R K	H L F . V Q D	P Q T	170	
R P Q P R S V P G W D S A	P G A P S P A D I T H		P A P G P S A		175	
P R R					191	
G G A					207	
M A E G G G Q N	H H E .	V V K F M	D V Y Q R S Y	C H P I E T L	V D	60
V S Q P D A P G	H Q R K	V V S W I	D V Y T R A T C C P R E	V V V	P	55
D E G L E C V P T	E E S N I	T M Q I M R I	K P H Q G Q H I	G E M S	121	
D D G L E C V P T	G Q H Q V	R M Q I L M I	Y P S S Q L	G E M S	115	
R Q E N P . . . . .	. . . . .	. . . . .	. . . . .	. . . . .	C	170
R P Q P R S V P G W D S A	P G A P S P A D I T H	P T P A P G P L			C	177
R C K A R Q L E L N	E R T C R C D K P R R					191
R C Q G R Q L E L N	P D T C R C K L R R					222

Fig 6(iii)

Fig. 6 (iii)

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Areas of 100% homology are boxed and conserved residues thought to be involved in homodimerisation are underlined. The VEGF sequence depicted includes the 26 amino acid leader sequence (removal of which gives rise to mature VEGF<sub>165</sub>) giving a total length of 191 amino acids.

Homology of SOM175 to VEGF<sub>165</sub> is 27% (33%) at the protein level, however within this are blocks of 100% homology. In particular, many structural residues are conserved including those thought to be involved in homodimerisation of VEGF (by comparison with PDGF).

ie. Cysteine-47

Proline-70, Cysteine-72, Valine-74

Arginine-77, Cystein-78, Glycine-80, Cysteines-81 & 82

Cysteine-89, Proline-91

Cysteines 122 & 124

Fig.6 (iii)

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SPLICE VARIANTS OF SOM175

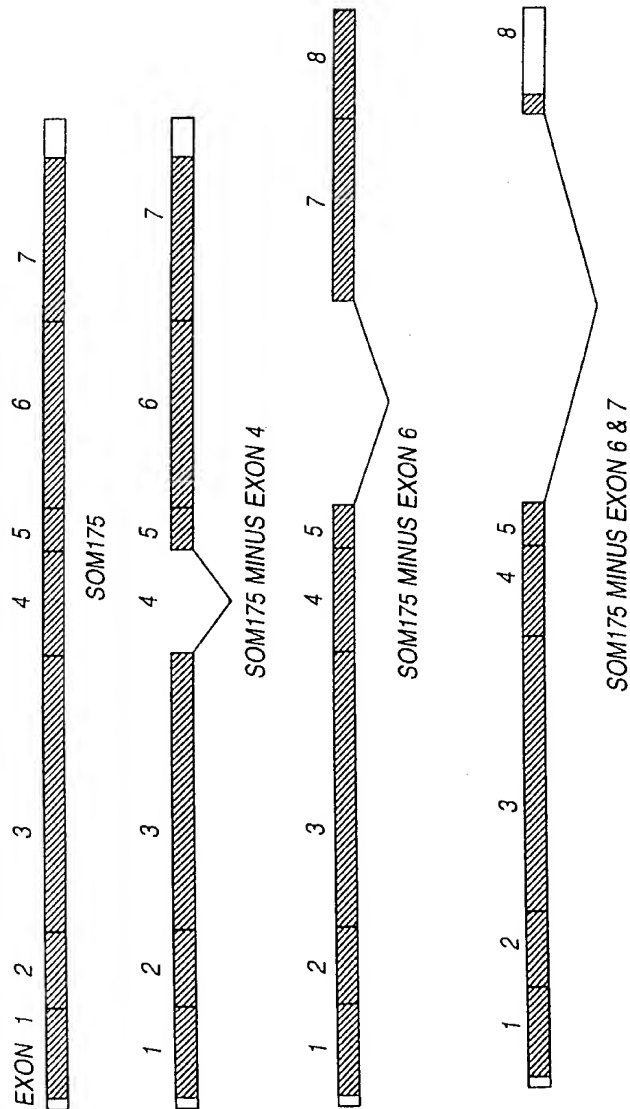


Fig.7



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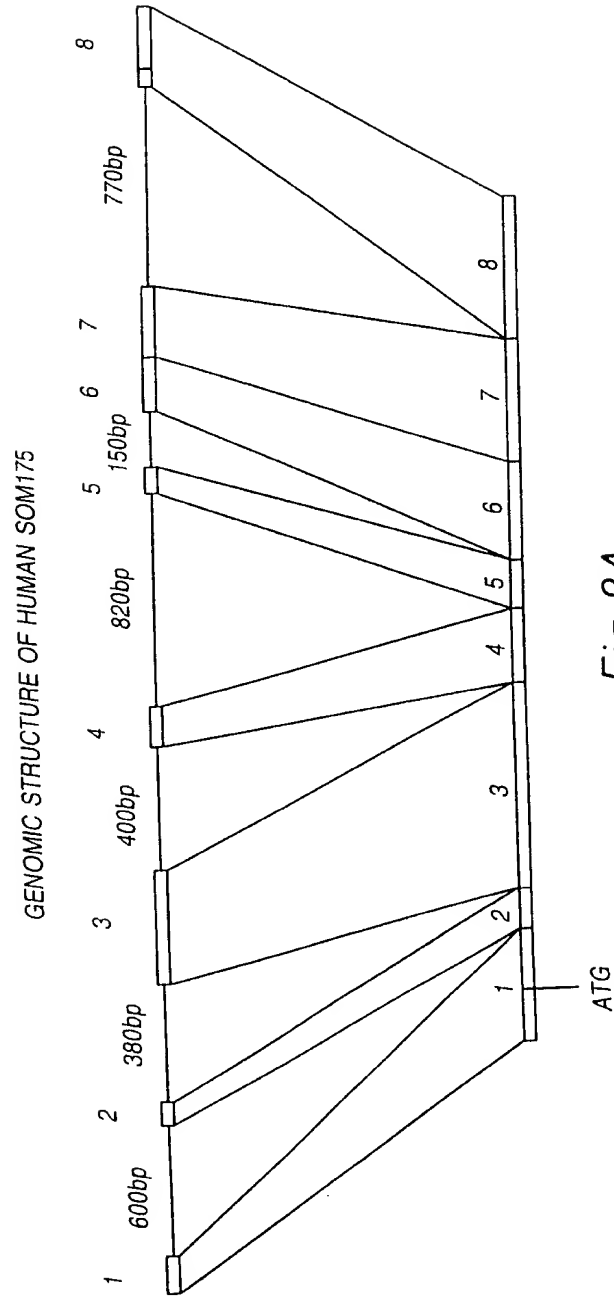


Fig.8A

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5'UTR...	<b>ATGAGG</b>	*Exon 1 (60bp)	GGCCAG	gtacgtgagg
tctccacacag	GCCCTT	Exon 2 (43bp)	GGAAAG	aatacttaca
tctgctccca	TGGTGT	Exon 3 (187bp)	ATGCAG	gtccgagatg
ctgaatacacag	ATCCTC	Exon 4 (73bp)	ATGCAG	gtgtcaggca
acttttcaag	ACCTAA	Exon 5 (34bp)	AGACAG	gtgagtctttt
ctcctccgta	GGCTGC	Exon 6 (101bp)	CTCCAG	ccccaggccc
cccactccag	CCCCAG	Exon 7 (109bp)	ACCCAG	acacctgtag
ccctgctcag	GTGCCG	*Exon 8 (22bp)	AGG <b>TGA</b>	...3'UTR

Fig.8B

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36/52  <i>Fig. 9(i)</i>	37/52  <i>Fig. 9(ii)</i>
38/52  <i>Fig. 9(iii)</i>	39/52  <i>Fig. 9(iv)</i>

Fig. 9

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-163 gcacgagctcaggccgctcgctgcggcgctg  
-103 gggggccgcggaggagccgccccctgcgcc  
-43 ggcggtctctggctgacccccccccacaccg

16 CGTCGCCTGCTGCTTGTGCACTGCTGCAG  
R R L L L V A L L Q

76 TTTGATGGCCCCAGTCACCAGAAGAAAGTG  
F D G P S H Q K K V

136 ACATGCCAGCCCAGGGAGGTGGTGGTGCCT  
T C Q P R E V V V P

196 AAACAACTAGTGCCCAGCTGTGTGACTGTG  
K Q L V P S C V T V

256 GGCCTGGAATGTGTGCCCAGTGGGCAACAC  
G L E C V P T G Q H

316 TACCCGAGCAGTCAGCTGGGGGAGATGTCC  
Y P S S Q L G E M S

376 CCTAAAAAAGGAGAGTGCTGTGAGGCCA  
P K K K E S A V R P

436 CAGCCCCGCTCTGTTCCGGGCTGGGACTCT  
Q P R S V P G W D S

Fig.9(i)

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cgttgcgctgcctgcgcccagggctcggga  
 ccgccccgggtccccgggtccgcgccaatgg  
 ccgggctagggcccgATGAGCCCCCTGCTG  
                                   M S P L L       -17  
                                   ↓  
 CTGGCTCGCACCCAGGCCCTGTGTCCCAG  
 L A R T Q A P V S Q       4  
  
 GTGCCATGGATAGACGTTTATGCACGTGCC  
 V P W I D V Y A R A       24  
  
 CTGAGCATGGAATCATGGGCAATGTGGTC  
 L S M E L M G N V V       44  
  
 CAGCGCTGTGGTGGCTGCTGCCCTGACGAT  
 Q R C G G C C P D D       64  
                                   ↓  
 CAAGTCCGAATGCAGATCCTCATGATCCAG  
 Q V R M Q I L M I Q       84  
  
 CTGGGAGAACACAGCCAATGTGAATGCAGA  
 L G E H S Q C E C R       104  
                                   ↓  
 GACAGGGTTGCCATACCCCACCACCGTCCC  
 D R V A I P H H R P       124  
  
ACCCCGGGAGCACCCCTCCCCAGCTGACATC  
 T P G A P S P A D I       144

Fig.9(ii)

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496 ATCCATCCCACTCCAGCCCCAGGATCCTCT  
I H P T P A P G S S  
S P R I L

556 CTGACCCCCGGACCTGCCGTTGCCGCTGTA  
L T P G P A V A A V  
P D P R T C R C R C

616 GGGGCTTAGAGCTCAACCCAGACACCTGTA  
G A \*  
R G L E L N P D T C

676 ctttccagactccacgggcccggctgcttt  
736 agcacaggcgtaacctcctcagtcctgggag  
796 gagctctctcgcctatcttttatctcccaga  
856 atgtctcacctcaggggccagggtactctc  
916 ttctggctggctgtctcccctcactatgaa  
976 gggttctgttatgataactgtgacacacac  
1036 gacactaaaaaaaaaaaaaaaaaaaaaaaaa

Fig.9(iii)

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GCCCGCCTTGCACCCAGCGCCGCCAACGCC  
A R L A P S A A N A 164  
C P P C T Q R R Q R 130

GACGCCGCGCTTCCTCCATTGCCAAGGGC  
D A A A S S I A K G 184  
R R R R F L H C Q G 150

↓  
GGTGCCGGAAGCCGCGAAAGTGAcaagctg 186  
R C R K P R K \* 167

tatggccctgcttcacagggagaagagtgg  
gtcactgccccaggacctggaccttttaga  
gctgccatctaacaattgtcaaggaacctc  
tcaacttaaccaccctgggtcaagtgagcatc  
aaccccaaacttctaccaataacgggattt  
acacactcacactctgataaaagagatgga  
aaaaaaaaaaaa

Fig.9(iv)

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Fig 10(i)	Fig 10(ii)



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A

hVRF167	-21	MSPLLRRLLLAALLQLAPAQAP	↓
mVRF167	-21	MSPLLRRLLLVALLQLARTQAP	
hVRF167	30	EVVVPLTVELMGTVAQLVPSC	
		:	
mVRF167	30	EVVVPLSMELMGNVVKQLVPSC	
hVRF167	80	ILMIRYPSSQLGEMSLEEHSQC	
		:	
mVRF167	80	ILMIQYPSSQLGEMSLGEHSQC	
hVRF167	130	RPDPRTCRCRCRRRSFLRCQGR	
		:	
mVRF167	130	RPDPRTCRCRCRRRFLHCQGR	

B

hVRF186	116	RAATPHHRPQPRSVPGWDSAPG
mVRF186	116	RVAIPHHRPQPRSVPGWDSTPG
hVRF186	166	TPGPAAAAADAAASSVAKGGA*
		:
mVRF186	166	TPGPAVAAVDAAASSIAKGGA*

Fig.10(i)

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VSQPDAPGHQRKVVSVIDVYTRATCQPR 29  
 ||| |:|:|:| | | | | | | | | |

VSQFDGPSHQKKVVPWIDVYARATCQPR 29

VTVQRCGGCCPDDGLECVPTGQHQVRMQ 79  
 | | | | | | | | | | | | | | | | | | | | | |

VTVQRCGGCCPDDGLECVPTGQHQVRMQ 79

ECRPKKKDSAVKPDSPRPLCPRCTQHHQ 129  
 | | | | | |:| |:| | | | | | | | | |:|

ECRPKKKESAVRPDSPRILCPPCTQRRQ 129

GLELNPDTCRCKLRR\* 167  
 | | | | | | | | | | | | | | | | | | | | | |

GLELNPDTCRCKPRK\* 167

APSPADITHPTPAPGPSAHAAPSTTSAL 165  
 | | | | | | | | | | | | | | | | | | | | | |

APSPADIIHPTPAPGSSARLAPSAANAL 165

186

186

Fig.10(ii)

FOI 2000-000000

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Fig 11(i)	Fig 11(ii)

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mVRF167	-21	MSPLLRRLLVALLQL..
		:   :
mVEGF188	-26	MNFLLSVHWTLALLLYLHH
mVRF167	25	TCQPREVVVPLSMELMGNVV
		:   :   : :
mVEGF188	24	YCRPIETLVDIFQEYPDEIE
mVRF167	75	QVRMQILMIQYPSSQ.LGEM
		:     :     :
mVEGF188	74	NITMQIMRIKPHQSQHIGEM
mVRF167	119	.....ILCPPC
		:
mVEGF188	124	QKRKRKKSFRKSWSVHCEPC
mVRF167	152	GLELNPDTCRCKPRK
		:
mVEGF188	173	QLELNERTCRCDKPRR

Fig.11(i)

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AR.TQAPVSQFDGPSHQKKVVPWIDVYARA	24
:   : :  : :  : ::	
AKWSQAAPT.T.EGEQKSHEVIKFMDVYQRS	23
KQLVPSCVTVQRCGGCCPDDGLECVPTGQH	74
:      :   :     ::      ::	
YIFKPSCVPLMRCAGCCNDEALECVPTSES	73
SLGEHSQCECRPKKESAVRPDSPR.....	118
: :	
SFLQHSRCECRPKKDRTPKPKSVRGKGKG	123
TQRRQR...PDPRTCRCRCRRRRFLHCQGR	151
:   :      :   : :  :	
SERRKHLFVQDPQTCKCCKNTDS.RCKAR	172
	167
	188

Fig.11(ii)

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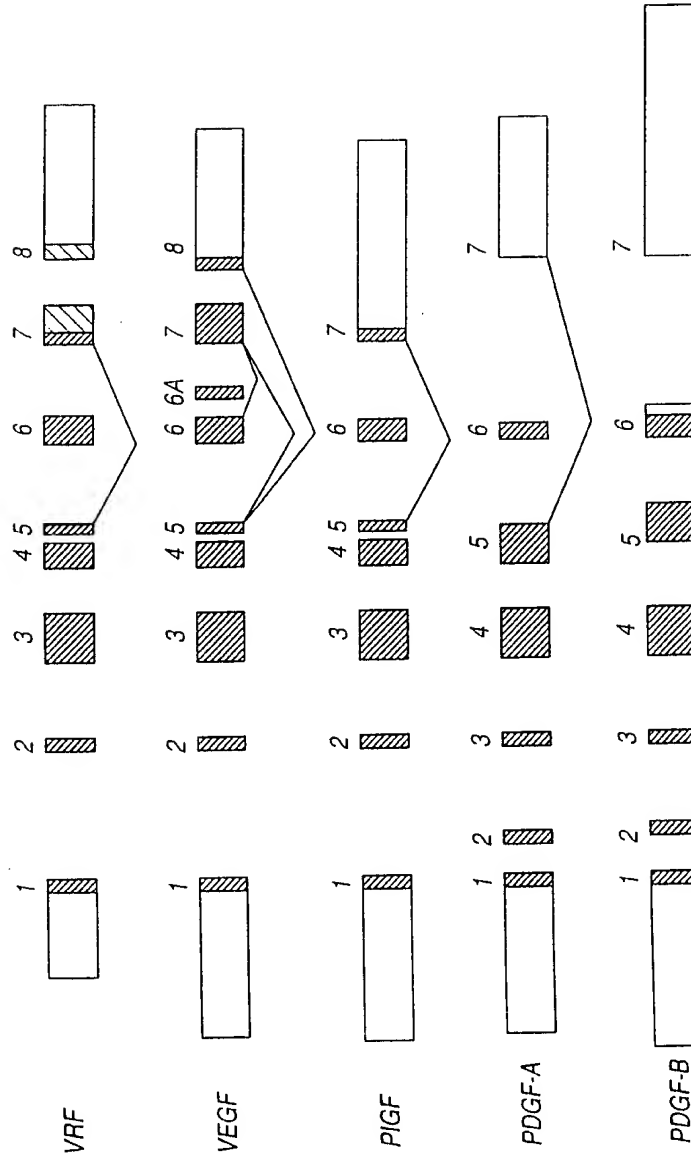
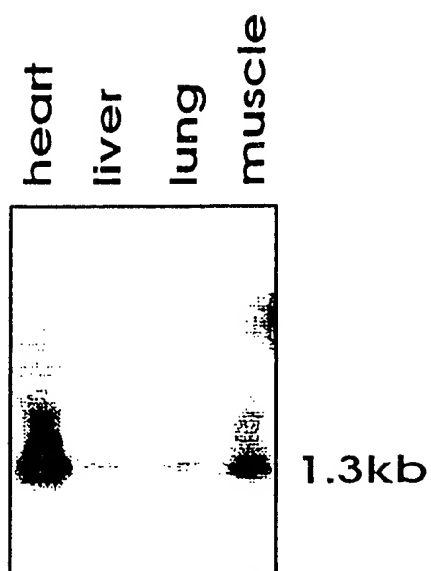


Fig.12

TOP SECRET (Date 26)

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*Fig.13*

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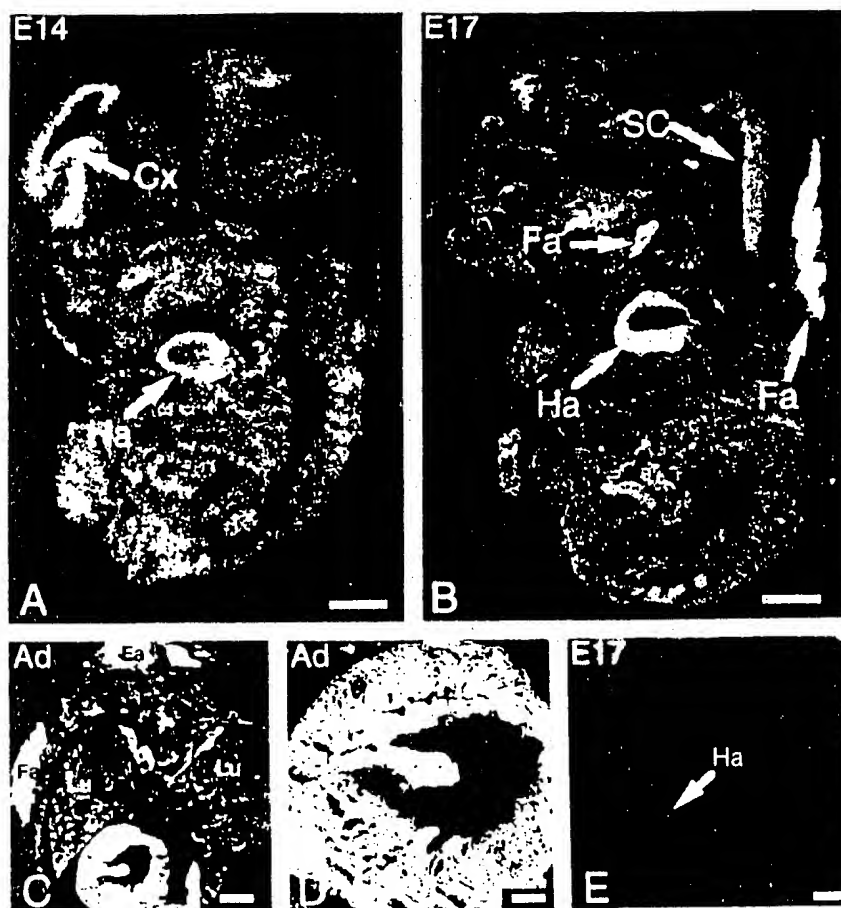


Fig.14



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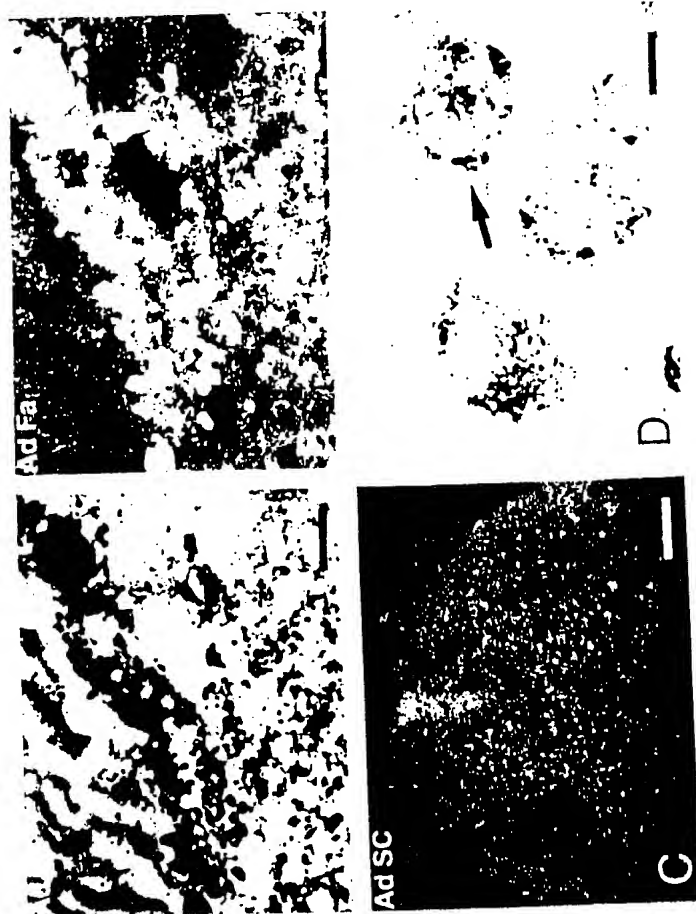


Fig.15

FIG. 15

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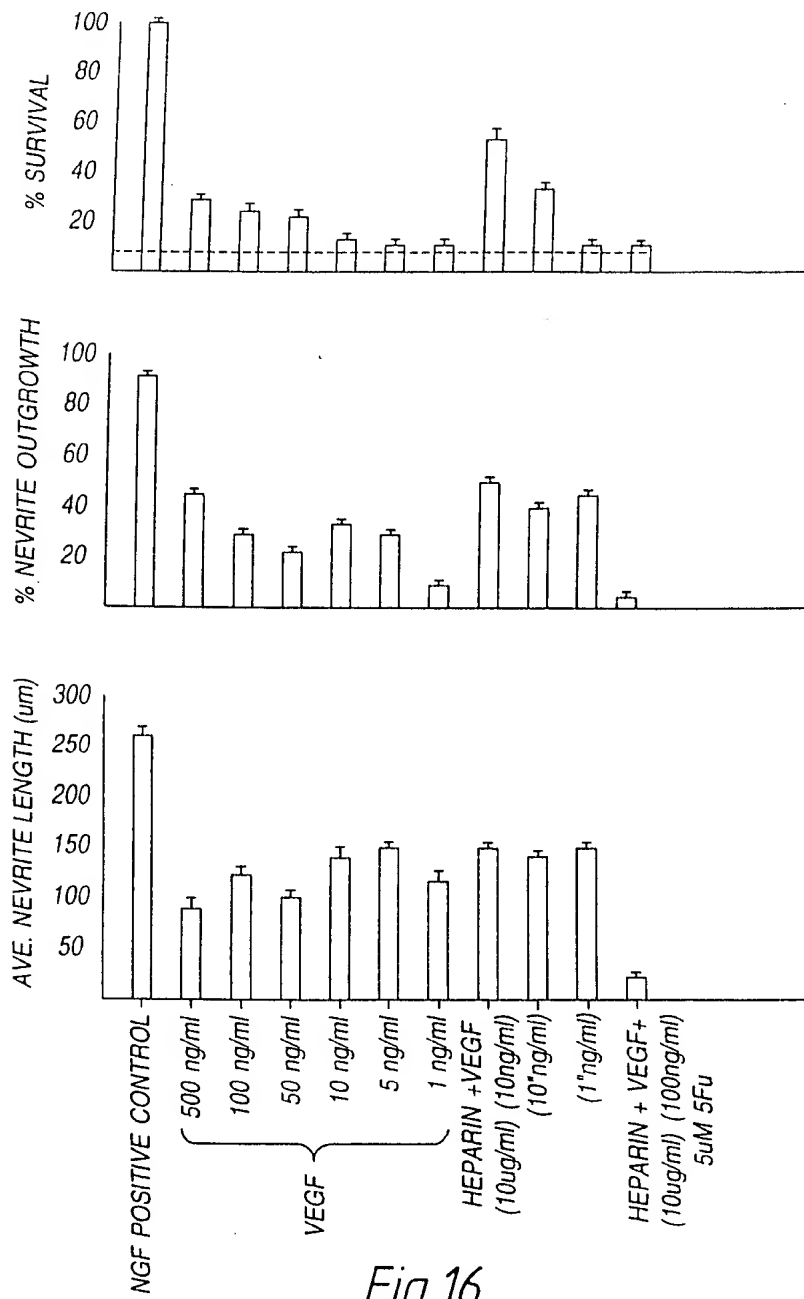


Fig.16

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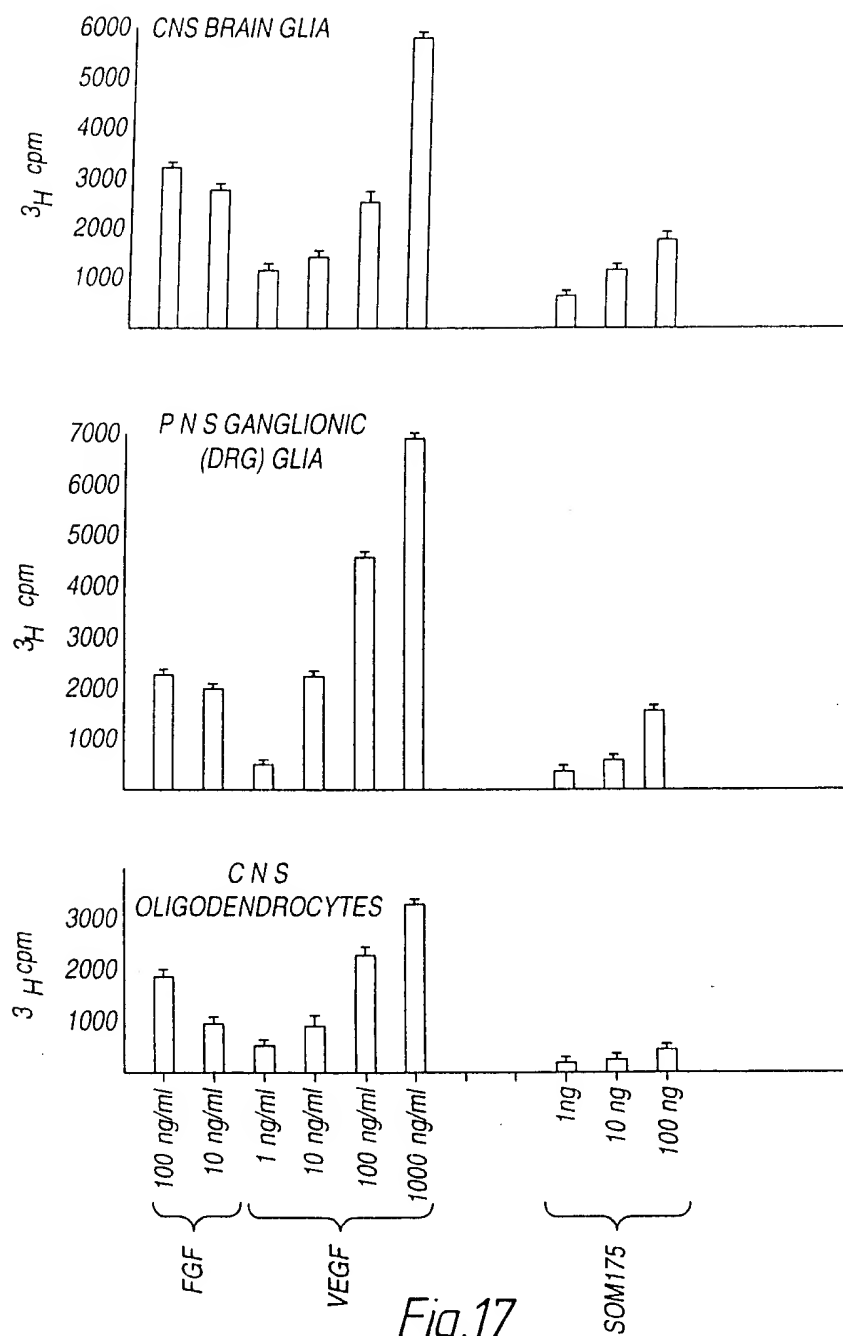


Fig.17

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## MOUSE ASTROGLIAL CELLS

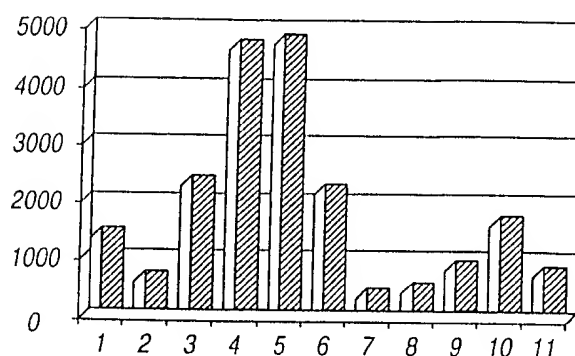


Fig.18

## MOUSE OLIGODENDROGLIAL CELLS

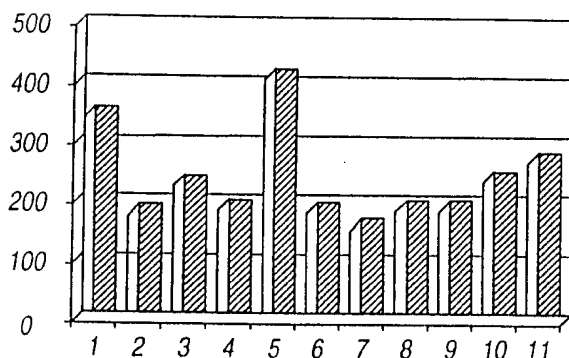


Fig.19

## MOUSE FOREBRAIN NEURONS

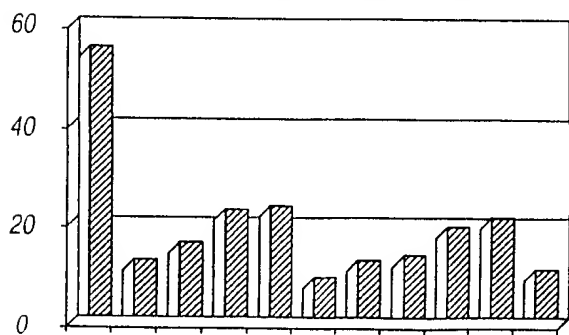


Fig.20